Figure 1: Shows an alignment between SEQ ID NO:9 translated sequence (SEQ ID NO:11) with *pha*A.

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Seq ID 9 B-ketothiolase Re   (1) MTRDVVIVSAVRTAIGTFGGSLKDIAPAELGAAVIKEALARAQVSGDDVG
             Our phaA         (1) -VTDVVIVSAARTAVGKFGGSLAKIPAPELGAAVVAALERAGVKPEQVS
             Consensus        (1)    DVVIVSA RTAIG FGGSL   I   ELGAALVIK AL RA V   D V

                                  51                                               100
Seq ID 9 B-ketothiolase Re  (51) HVLPGAVEQTEPRDMYLARVAADNGCGTINAPAMTINRICGSGLQAFMSA
             Our phaA        (50) EVIMGCVPTAGS-GQNPARQAAIKAGIPAMVPAMTINRICGSGLKAVMLA
             Consensus       (51) VI GNVI        AR AAI AGL       PALTINKLCGSGL AIM A

                                  101                                              150
Seq ID 9 B-ketothiolase Re (101) ARTIALGDTIIAIAGGQAESMSRAPCKAFAPYKWGARMGDAGLVDMMIG-EL
             Our phaA        (99) ANAIIAGDAEVVGGQENMSAAPHVLPGSRDGFRMGDAKLVDTMIVDGL
             Consensus      (101) AN IL GD DI IAGG E MS APHL PAAR G RMGDA LVD MI   AL

                                  151                                              200
Seq ID 9 B-ketothiolase Re (150) HDPMHRIHMGITAENVAKEYDIERAQQDEAAIESHRQASAAIKAGYFKDQ
             Our phaA       (149) WDVMNQYHMGITAENVAKEYGISREAQDEFAVGSQNIAEAAQKAGKFDEE
             Consensus      (151)  D F  HMGITAENVAKEY ISR QDE AL S  KA AA KAG F D

                                  201                                              250
Seq ID 9 B-ketothiolase Re (200) IVPVMSKGRK-GDVTFDTDEHVRHDATIDDMIKLRPVFVKENGTVTAINA
             Our phaA       (199) IVPVIIPQRKGDPVAFKTDEFVRQGATLDSMEGLSPAFDK-AGTVTAINA
             Consensus      (201) IVPVL   RK   V F TDE VR  ATID MS LKP F K  GTVTAANA

                                  251                                              300
Seq ID 9 B-ketothiolase Re (249) SGLNDGAAAVVZMERAEAERRGLKPLAREVSYSHAGVDPKAMGGGPVPAI
             Our phaA       (248) SGLNDGAAAVVIMSAAKAKELGL/TPLATIKSYIANAGVDPKVMGGGPVPAS
             Consensus      (251) SGLNDAAAAVVMM  A A   GL PLA I SYA AGVDPK MGIGPVPAS

                                  301                                              350
Seq ID 9 B-ketothiolase Re (299) KIALERAGLQVSDLDVVEANEAFAAQACAVTKAGLDPKVNPNGGSIISI
             Our phaA       (298) KRALSRAEWTPQDLDLVMEINEAFAAQALAVHQQYGWDTSKVNVNGGGTEAI
             Consensus      (301) K AL RA    DLDLIE NEAFAAQA AV   LG D AKVN NG AIAI

                                  351                                              397
Seq ID 9 B-ketothiolase Re (349) GHPIGAIGALITVKALHEINRVQERYELVIMCIGIFERI-------
             Our phaA       (348) GHPIGAIGCRILVTLLHEIKRRDZIKALASICISGMGVALAVERK-
             Consensus      (351) GHPIGASG  I V  LHEL R  AK AL SLCIAA
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